

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Koopman, Peter  
Goodfellow, Peter
- (ii) TITLE OF THE INVENTION: SOX-9 GENE AND PROTEIN AND  
USE IN THE REGENERATION OF BONE OR CARTILAGE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Scully, Scott, Murphy & Presser  
(B) STREET: 400 Garden City Plaza  
(C) CITY: Garden City  
(D) STATE: NY  
(E) COUNTRY: U.S.A.  
(F) ZIP: 11530
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/860,635  
(B) FILING DATE: 29-MAY-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: AU PM9714  
(B) FILING DATE: 29-NOV-1994  
  
(A) APPLICATION NUMBER: AU PM9835  
(B) FILING DATE: 05-DEC-1994  
  
(A) APPLICATION NUMBER: PCT/AU95/00799  
(B) FILING DATE: 29-NOV-1995
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: DiGiglio, Frank S.  
(B) REGISTRATION NUMBER: 31,346  
(C) REFERENCE/DOCKET NUMBER: 10981
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 516-742-4343  
(B) TELEFAX: 516-742-4366  
(C) TELEX:

FILED " 48001600

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTAAA

7

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCAAAGTCCT AAAGGTGGG

19

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTCAGGCAA ATAAGGCAG

19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGGCAATCTA ACAGATGAGA

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCNCAAATGT CATATATCCA

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTCCAGATT GACTGGAACA CA

22

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAATAAGAT ACTAATATGT AGAG

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCAGCAGAA ATCCTAAAGG

20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAATGCC GATGGTTAAG

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCCTCGAGG TGGCTTATCG

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCATACACA TACGATTTAG GTGAC

25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGGAAGTCG GTGAAGAAC

19

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCGCTCATGC CGGAGGAGGA G

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCAATCCCAG GGCCCACCGA C

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTGGAGATGA CGTCGACTGC TC

22

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCAGCGACGT CATCTCCAAC

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGCTTGA CATCCACAG T

21

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2249 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTTTCAGTC	CAGGAAC TTT	TCTTTGCAAG	AGAGACGAGG	TGCAAGTGGC	50
CCCGGTTTCG	TTCTCTGTTT	TCCCTCCCTC	CTCCTCCGCT	CCGACTCGCC	100
TTCCCCGGGT	TTAGAGCCGG	CAGCTGAGAC	CCGCCACCCA	GCGCCTCTGC	150
TAAGTGCCCC	CCGCCGCAGC	CCGGTGACGC	GCCAACCTCC	CCGGGAGCCG	200
TTGCTCGGC	GTCCGCGTCC	GGGCAGCTGA	GGGAAGAGGA	GCCCCAGCCG	250
CCGCGGCTTC	TCGCCTTTCC	CGGCCACCCG	CCCCCTGCCC	CGGGCTCGCG	300
TATGAATCTC	CTGGACCCCT	TCATGAAGAT	GACCGACGAG	CAGGAGAAGG	350
GCCTGTCTGG	CGCCCCCAGC	CCCACCATGT	CGGAGGACTC	GGCTGGTTCG	400
CCCTGTCCCT	CGGGCTCCGG	CTCGGACACG	GAGAACACCC	GGCCCCAGGA	450
GAACACCTTC	CCCAAGGGCG	AGCCGGATCT	GAAGAAGGAG	AGCGAGGAAG	500
ATAAGTTCCC	CGTGTGCATC	CGCGAGGCGG	TCAGCCAGGT	GCTGAAGGGC	550
TACGACTGGA	CGCTGGTGCC	CATGCCCGTG	CGCGTCAACG	GCTCCAGCAA	600
GAACAAGCCA	CACGTCAAGC	GACCCATGAA	CGCCTTCATG	GTGTGGGCGC	650
AGGCTGCGCG	CAGGAAGCTG	GCAGACCAGT	ACCCGCATCT	GCACAACGCG	700
GAGCTCAGCA	AGACTCTGGG	CAAGCTCTGG	AGGCTGCTGA	ACGAGAGCGA	750
GAAGAGACCC	TTCGTGGAGG	AGGCGGAGCG	GCTGCGCGTG	CAGCACAAGA	800
AAGACCACCC	CGATTACAAG	TACCAGCCCC	GGCGGAGGAA	GTCGGTGAAG	850
AACGGACAAG	CGGAGGCCGA	AGAGGCCACG	GAACAGACTC	ACATCTCTCC	900
TAATGCTATC	TTCAAGGCGC	TGCAAGCCGA	CTCCCCACAT	TCCTCCTCCG	950
GCATGAGTGA	GGTGC ACTCC	CCGGGCGAGC	ACTCTGGGCA	ATCTCAGGGT	1000
CCGCCGACCC	CACCCACCAC	TCCCAAAACC	GACGTGCAAG	CTGGCAAAGT	1050
TGATCTGAAG	CGAGAGGGGC	GCCCTCTGGC	AGAGGGGGGC	AGACAGCCCC	1100
CCATCGACTT	CCGCGACGTG	GACATCGGTG	AACTGAGCAG	CGACGTCATC	1150
TCCAACATTG	AGACCTTCGA	CGTCAATGAG	TTTGACCAAT	ACTTGCCACC	1200
CAACGGCCAC	CCAGGGGTTC	CGGCCACCCA	CGGCCAGGTC	ACCTACACTG	1250
GCAGTTACGG	CATCAGCAGC	ACCGCACCCA	CCCCTGCGAC	CGCGGGCCAC	1300
GTGTGGATGT	CGAAGCAGCA	GGCGCCGCCC	CCTCCTCCGC	AGCAGCCTCC	1350
GCAGGCCCCG	CAAGCCCCAC	AGGCGCCTCC	GCAGCAGCAA	GCACCCCGCG	1400

AGCAGCCGCA	GGCACCCCAG	CAGCAGCAGG	CACACACGCT	CACCACGCTG	1450
AGCAGCGAGC	CAGGCCAGTC	CCAGCGAACG	CACATCAAGA	CGGAGCAGCT	1500
GAGCCCCAGC	CACTACAGGG	AGCAGCAGCA	GCACTCCCCG	CAACAGATCT	1550
CCTACAGCCC	CTTCAACCTT	CCTCACTACA	GGCCCTCCTA	CCCGCCCATC	1600
ACCCGTTCGG	AATACGACTA	CGCTGACCAT	CAGAACTCCG	GCTCCTACTA	1650
CAGTCACGCA	GCCGGCCAGG	GCTCAGGGCT	CTACTCCACC	TTCACTTACA	1700
TGAACCCCGC	GCAGCGCCCC	ATGTACACCC	CCATCGGTGA	CACCTCCGGG	1750
GTCCCTTCCA	TCCCGCAGAC	CCACAGCCCG	CAGGACTGGG	AACAACCACT	1800
CTACACACAG	GTCACCAGAC	CCTGAGAAGA	GAAAAGCTAT	GGTGACAGAG	1850
CTGATCTTTT	TTTTTTTTTT	TTTTTAAAGA	AGAAAAGAAA	GAAACGAAAA	1900
AGAAAAAGCT	GAAGGAAATC	AAGAACCAAT	TGAAATTCCT	TTGGACACTT	1950
TTTTTTTTTGT	CCTTTCGTTA	ATTTTAAAAA	GACATGTAAA	GGAAGGTAAC	2000
GATTGCTGGG	CATTCCAGGA	GAGAGACTTT	AAGACTTTGT	CTGAGCTCAT	2050
GACAACATAT	TGCAAAATGGC	CGGGCCACTC	GTGGCCAGAC	GGACAGCACT	2100
CCTGGCCAGA	TGGACCCACC	AGTATCAGCG	AGGAGGGGCT	TGTCTCCTTC	2150
AGAGTTAACA	TGGAGGACGA	TTGGAGAATC	TCCCTGCCTG	TTTGGACTTT	2200
GTAATTATTT	TTTAGCCGTA	ATTAAAGAAA	AAAAAAGTCC	AAAAAAAAAA	2249

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Asn	Leu	Leu	Asp	Pro	Phe	Met	Lys	Met	Thr	Asp	Glu	Gln	Glu	Lys
1				5				10						15	
Gly	Leu	Ser	Gly	Ala	Pro	Ser	Pro	Thr	Met	Ser	Glu	Asp	Ser	Ala	Gly
			20					25					30		
Ser	Pro	Cys	Pro	Ser	Gly	Ser	Gly	Ser	Asp	Thr	Glu	Asn	Thr	Arg	Pro
		35					40					45			



Gln 50	Glu	Asn	Thr	Phe	Pro	Lys 55	Gly	Glu	Pro	Asp	Leu 60	Lys	Lys	Glu	Ser
Glu 65	Glu	Asp	Lys	Phe	Pro 70	Val	Cys	Ile	Arg	Glu 75	Ala	Val	Ser	Gln	Val 80
Leu	Lys	Gly	Tyr	Asp 85	Trp	Thr	Leu	Val	Pro 90	Met	Pro	Val	Arg	Val 95	Asn
Gly	Ser	Ser	Lys 100	Asn	Lys	Pro	His	Val 105	Lys	Arg	Pro	Met	Asn 110	Ala	Phe
Met	Val	Trp 115	Ala	Gln	Ala	Ala	Arg 120	Arg	Lys	Leu	Ala	Asp 125	Gln	Tyr	Pro
His	Leu 130	His	Asn	Ala	Glu	Leu 135	Ser	Lys	Thr	Leu	Gly 140	Lys	Leu	Trp	Arg
Leu 145	Leu	Asn	Glu	Ser	Glu 150	Lys	Arg	Pro	Phe	Val 155	Glu	Glu	Ala	Glu	Arg 160
Leu	Arg	Val	Gln	His 165	Lys	Lys	Asp	His	Pro 170	Asp	Tyr	Lys	Tyr	Gln 175	Pro
Arg	Arg	Arg	Lys 180	Ser	Val	Lys	Asn	Gly 185	Gln	Ala	Glu	Ala	Glu 190	Glu	Ala
Thr	Glu	Gln 195	Thr	His	Ile	Ser	Pro 200	Asn	Ala	Ile	Phe	Lys 205	Ala	Leu	Gln
Ala	Asp 210	Ser	Pro	His	Ser	Ser 215	Ser	Gly	Met	Ser	Glu 220	Val	His	Ser	Pro
Gly 225	Glu	His	Ser	Gly	Gln 230	Ser	Gln	Gly	Pro	Pro 235	Thr	Pro	Pro	Thr	Thr 240
Pro	Lys	Thr	Asp	Val 245	Gln	Ala	Gly	Lys	Val 250	Asp	Leu	Lys	Arg	Glu 255	Gly
Arg	Pro	Leu	Ala 260	Glu	Gly	Gly	Arg	Gln 265	Pro	Pro	Ile	Asp	Phe 270	Arg	Asp
Val	Asp 275	Ile	Gly	Glu	Leu	Ser	Ser 280	Asp	Val	Ile	Ser	Asn 285	Ile	Glu	Thr
Phe	Asp 290	Val	Asn	Glu	Phe	Asp 295	Gln	Tyr	Leu	Pro	Pro 300	Asn	Gly	His	Pro
Gly 305	Val	Pro	Ala	Thr	His 310	Gly	Gln	Val	Thr	Tyr 315	Thr	Gly	Ser	Tyr	Gly 320
Ile	Ser	Ser	Thr	Ala 325	Pro	Thr	Pro	Ala	Thr 330	Ala	Gly	His	Val	Trp 335	Met
Ser	Lys	Gln	Gln 340	Ala	Pro	Pro	Pro	Pro 345	Pro	Gln	Gln	Pro	Pro 350	Gln	Ala

the effect of the high level of the  $\alpha$  parameter on the results of the model. The results show that the high level of the  $\alpha$  parameter leads to a higher level of the  $\beta$  parameter, which in turn leads to a higher level of the  $\gamma$  parameter. This is because the high level of the  $\alpha$  parameter leads to a higher level of the  $\beta$  parameter, which in turn leads to a higher level of the  $\gamma$  parameter.

Pro Gln Ala Pro Gln Ala Pro Pro Gln Gln Gln Ala Pro Pro Gln Gln  
355 360 365

Pro Gln Ala Pro Gln Gln Gln Gln Ala His Thr Leu Thr Thr Leu Ser  
370 375 380

Ser Glu Pro Gly Gln Ser Gln Arg Thr His Ile Lys Thr Glu Gln Leu  
385 390 395 400

Ser Pro Ser His Tyr Arg Glu Gln Gln Gln His Ser Pro Gln Gln Ile  
405 410 415

Ser Tyr Ser Pro Phe Asn Leu Pro His Tyr Arg Pro Ser Tyr Pro Pro  
420 425 430

Ile Thr Arg Ser Glu Tyr Asp Tyr Ala Asp His Gln Asn Ser Gly Ser  
435 440 445

Tyr Tyr Ser His Ala Ala Gly Gln Gly Ser Gly Leu Tyr Ser Thr Phe  
450 455 460

Thr Tyr Met Asn Pro Ala Gln Arg Pro Met Tyr Thr Pro Ile Gly Asp  
465 470 475 480

Thr Ser Gly Val Pro Ser Ile Pro Gln Thr His Ser Pro Gln Asp Trp  
485 490 495

Glu Gln Pro Val Tyr Thr Gln Val Thr Arg Pro  
500 505

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3923 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGAGCTCGA AACTGACTGG AAACCTTCAGT GGCGCGGAGA CTCGCCAGTT TCAACCCCGG	60
AAACTTTTCT TTGCAGGAGG AGAAGAGAAG GGGTGCAAGC GCCCCCACTT TTGCTCTTTT	120
TCCTCCCCTC CTCCTCCTCT CCAATTCGCC TCCCCCACT TGGAGCGGGC AGCTGTGAAC	180
TGGCCACCCC GCGCCTTCCT AAGTGCTCGC CGCGGTAGCC GGCCGACGCG CCAGCTTCCC	240
CGGGAGCCGC TTGCTCCGCA TCCGGGCAGC CGAGGGGAGA GGAGCCCGCG CCTCGAGTCC	300
CCGAGCCGCC GCGGCTTCTC GCCTTTCCCG GCCACCAGCC CCCTGCCCCG GGCCCGCGTA	360
TGAATCTCCT GGACCCCTTC ATGAAGATGA CCGACGAGCA GGAGAAGGGC CTGTCCGGCG	420

CCCCCAGCCC	CACCATGTCC	GAGGACTCCG	CGGGCTCGCC	CTGCCCCTCG	GGCTCCGGCT	480
CGGACACCGA	GAACACGCGG	CCCCAGGAGA	ACACGTTCCC	CAAGGGCGAG	CCCGATCTGA	540
AGAAGGAGAG	CGAGGAGGAC	AAGTTCCCCG	TGTGCATCCG	CGAGGCGGTC	AGCCAGGTGC	600
TCAAAGGCTA	CGACTGGACG	CTGGTGCCCA	TGCCGGTGCG	CGTCAACGGC	TCCAGCAAGA	660
ACAAGCCGCA	CGTCAAGCGG	CCCATGAACG	CCTTCATGGT	GTGGGCGCAG	GCGGCGCGCA	720
GGAAGCTCGC	GGACCAGTAC	CCGCACTTGC	ACAACGCCGA	GCTCAGCAAG	ACGCTGGGCA	780
AGCTCTGGAG	ACTTCTGAAC	GAGAGCGAGA	AGCGGCCCTT	CGTGGAGGAG	GCGGAGCGGC	840
TGCGCGTGCA	GCACAAGAAG	GACCACCCGG	ATTACAAGTA	CCAGCCGCGG	CGGAGGAAGT	900
CGGTGAAGAA	CGGGCAGGCG	GAGGCAGAGG	AGGCCACGGA	GCAGACGCAC	ATCTCCCCCA	960
ACGCCATCTT	CAAGGCGCTG	CAGGCCGACT	CGCCACACTC	CTCCTCCGGC	ATGAGCGAGG	1020
TGCACTCCCC	CGGCGAGCAC	TCGGGGCAAT	CCCAGGGCCC	ACCGACCCCA	CCCACCACCC	1080
CCAAAACCGA	CGTGCAGCCG	GGCAAGGCTG	ACCTGAAGCG	AGAGGGGCGC	CCCTTGCCAG	1140
AGGGGGGCGAG	ACAGCCCCCT	ATCGACTTCC	GCGACGTGGA	CATCGGCGAG	CTGAGCAGCG	1200
ACGTCATCTC	CAACATCGAG	ACCTTCGATG	TCAACGAGTT	TGACCAGTAC	CTGCCGCCCA	1260
ACGGCCACCC	GGGGGTGCCG	GCCACGCACG	GCCAGGTCAC	CTACACGGGC	AGCTACGGCA	1320
TCAGCAGCAC	CGCGGCCACC	CCGGCGAGCG	CGGGCCACGT	GTGGATGTCC	AAGCAGCAGG	1380
CGCCGCCGCC	ACCCCCGCAG	CAGCCCCCAC	AGGCCCCGCC	GGCCCCGCAG	GCGCCCCCGC	1440
AGCCGCAGGC	GGCGCCCCCA	CAGCAGCCGG	CGGCACCCCC	GCAGCAGCCA	CAGGCGCACA	1500
CGCTGACCAC	GCTGAGCAGC	GAGCCGGGCC	AGTCCCAGCG	AACGCACATC	AAGACGGAGC	1560
AGCTGAGCCC	CAGCCACTAC	AGCGAGCAGC	AGCAGCACTC	GCCCCAACAG	ATCGCCTACA	1620
GCCCCTTCAA	CCTCCCACAC	TACAGCCCCT	CCTACCCGCC	CATCACCCGC	TCACAGTACG	1680
ACTACACCGA	CCACCAGAAC	TCCAGCTCCT	ACTACAGCCA	CGCGGCAGGC	CAGGGCACCG	1740
GCCTCTACTC	CACCTTCACC	TACATGAACC	CCGCTCAGCG	CCCCATGTAC	ACCCCCATCG	1800
CCGACACCTC	TGGGGTCCCT	TCCATCCCGC	AGACCCACAG	CCCCCAGCAC	TGGGAACAAC	1860
CCGTCTACAC	ACAGCTCACT	CGACCTTGAG	GAGGCCTCCC	ACGAAGGGCG	ACGATGGCCG	1920
AGATGATCCT	AAAAATAACC	GAAGAAAGAG	AGGACCAACC	AGAATTCCCT	TTGGACATTT	1980
GTGTTTTTTT	GTTTTTTTAT	TTTGTTTTGT	TTTTTCTTCT	TCTTCTTCTT	CCTTAAAGAC	2040
ATTTAAGCTA	AAGGCAACTC	GTACCCAAAT	TTCCAAGACA	CAAACATGAC	CTATCCAAGC	2100

GCATTACCCA	CTTGTGGCCA	ATCAGTGGCC	AGGCCAACCT	TGGCTAAATG	GAGCAGCGAA	2160
ATCAACGAGA	AACTGGACTT	TTTAAACCCT	CTTCAGAGCA	AGCGTGGAGG	ATGATGGAGA	2220
ATCGTGTGAT	CAGTGTGCTA	AATCTCTCTG	CCTGTTTGGA	CTTTGTAATT	ATTTTTTTTAG	2280
CAGTAATTAA	AGAAAAAAGT	CCTCTGTGAG	GAATATTCTC	TATTTTAAAT	ATTTTTTAGTA	2340
TGTACTGTGT	ATGATTCATT	ACCATTTTGA	GGGGATTTAT	ACATATTTTT	AGATAAAATT	2400
AAATGCTCTT	ATTTTTTCCAA	CAGCTAAACT	ACTCTTAGTT	GAACAGTGTG	CCCTAGCTTT	2460
TCTTGCAACC	AGAGTATTTT	TGTACAGATT	TGCTTTCTCT	TACAAAAAGA	AAAAAAAAAAT	2520
CCTGTTGTAT	TAACATTTAA	AAACAGAATT	GTGTTATGTG	ATCAGTTTTG	GGGGTTAACT	2580
TTGCTTAATT	CCTCAGGCTT	TGCGATTTAA	GGAGGAGCTG	CCTTAAAAAA	AAATAAAGGC	2640
CTTATTTTGC	AATTATGGGA	GTAAACAATA	GTCTAGAGAA	GCATTTGGTA	AGCTTTTATGA	2700
TATATATATT	TTTTAAAGAA	GAGAAAAACA	CCTTGAGCCT	TAAACGGTG	CTGCTGGGAA	2760
ACATTTGCAC	TCTTTTAGTG	CATTTCTCTC	TGCCTTTGCT	TGTTCACTGC	AGTCTTAAGA	2820
AAGAGGTAAA	AGGCAAGCAA	AGGAGATGAA	ATCTGTTCTG	GGAATGTTTC	AGCAGCCAAT	2880
AAGTGCCCGA	GCACACTGCC	CCCGGTTGCC	TGCCTGGGCC	CCATGTGGAA	GGCAGATGCC	2940
TGCTCGCTCT	GTCACCTGTG	CCTCTCAGAA	CACCAGCAGT	TAACCTTCAA	GACATTCCAC	3000
TTGCTAAAAT	TATTTATTTT	GTAAGGAGAG	GTTTTAATTA	AAACAAAAAA	AAATTCTTTT	3060
TTTTTTTTTT	TTTTCCAATT	TTACCTTCTT	TAAAATAGGT	TGTTGGAGCT	TTCCTCAAAG	3120
GGTATGGTCA	TCTGTTGTTA	AATTATGTTC	TTAACTGTAA	CCAGTTTTTT	TTTATTTATC	3180
TCTTTAATCT	TTTTTATTAT	TAAAAGCAAG	TTTCTTTGTA	TTCCTCACCC	TAGATTTGTA	3240
TAAATGCCTT	TTTGTCCATC	CCTTTTTTCT	TTGTTGTTTT	TGTTGAAAAC	AAACTGGAAA	3300
CTTGTTTCTT	TTTTTGTATA	AATGAGAGAT	TGCAAATGTA	GTGTATCACT	GAGTCATTTG	3360
CAGTGTTTTTC	TGCCACAGAC	CTTTGGGCTG	CCTTATATTG	TGTGTGTGTG	TGGGTGTGTG	3420
TGTGTTTTGA	CACAAAAACA	ATGCAAGCAT	GTGTCATCCA	TATTTCTCTA	CATCTTCTCT	3480
TGGAGTGAGG	GAGGCTACCT	GGAGGGGATC	AGCCCACTGA	CAGACCTTAA	TCTTAATTAC	3540
TGCTGTGGCT	AGAGAGTTTG	AGGATTGCTT	TTTAAAAAAG	ACAGCAAAC	TTTTTTTTTA	3600
TTTAAAAAAA	GATATATTAA	CAGTTTTAGA	AGTCAGTAGA	ATAAAATCTT	AAAGCACTCA	3660
TAATATGGCA	TCCTTCAATT	TCTGTATAAA	AGCAGATCTT	TTTAAAAAAG	ATACTTCTGT	3720
AACTTAAGAA	ACCTGGCATT	TAAATCATAT	TTTGTCTTTA	GGTAAAAGCT	TTGGTTTGTG	3780

TTCGTGTTTT	GTTTGTTC	CTTGTTTCCC	TCCCAGCCCC	AAACCTTTTG	TTCTCTCCGT	3840
GAAACTTACC	TTTCCCTTTT	TCTTTCTCTT	TTTTTTTTTG	TATATTATTG	TTTACAATAA	3900
ATATACATTG	CATTAAAAAG	AAA				3923

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Asn	Leu	Leu	Asp	Pro	Phe	Met	Lys	Met	Thr	Asp	Glu	Gln	Glu	Lys
1				5					10					15	
Gly	Leu	Ser	Gly	Ala	Pro	Ser	Pro	Thr	Met	Ser	Glu	Asp	Ser	Ala	Gly
			20					25					30		
Ser	Pro	Cys	Pro	Ser	Gly	Ser	Gly	Ser	Asp	Thr	Glu	Asn	Thr	Arg	Pro
		35					40					45			
Gln	Glu	Asn	Thr	Phe	Pro	Lys	Gly	Glu	Pro	Asp	Leu	Lys	Lys	Glu	Ser
	50					55					60				
Glu	Glu	Asp	Lys	Phe	Pro	Val	Cys	Ile	Arg	Glu	Ala	Val	Ser	Gln	Val
65					70					75				80	
Leu	Lys	Gly	Tyr	Asp	Trp	Thr	Leu	Val	Pro	Met	Pro	Val	Arg	Val	Asn
				85					90					95	
Gly	Ser	Ser	Lys	Asn	Lys	Pro	His	Val	Lys	Arg	Pro	Met	Asn	Ala	Phe
			100					105					110		
Met	Val	Trp	Ala	Gln	Ala	Ala	Arg	Arg	Lys	Leu	Ala	Asp	Gln	Tyr	Pro
		115					120					125			
His	Leu	His	Asn	Ala	Glu	Leu	Ser	Lys	Thr	Leu	Gly	Lys	Leu	Trp	Arg
	130					135					140				
Leu	Leu	Asn	Glu	Ser	Glu	Lys	Arg	Pro	Phe	Val	Glu	Glu	Ala	Glu	Arg
145					150					155					160
Leu	Arg	Val	Gln	His	Lys	Lys	Asp	His	Pro	Asp	Tyr	Lys	Tyr	Gln	Pro
				165					170					175	
Arg	Arg	Arg	Lys	Ser	Val	Lys	Asn	Gly	Gln	Ala	Glu	Ala	Glu	Glu	Ala
			180					185					190		
Thr	Glu	Gln	Thr	His	Ile	Ser	Pro	Asn	Ala	Ile	Phe	Lys	Ala	Leu	Gln
	195						200					205			
Ala	Asp	Ser	Pro	His	Ser	Ser	Ser	Gly	Met	Ser	Glu	Val	His	Ser	Pro
	210					215					220				
Gly	Glu	His	Ser	Gly	Gln	Ser	Gln	Gly	Pro	Pro	Thr	Pro	Pro	Thr	Thr
225					230				235					240	
Pro	Lys	Thr	Asp	Val	Gln	Pro	Gly	Lys	Ala	Asp	Leu	Lys	Arg	Glu	Gly
			245					250						255	
Arg	Pro	Leu	Pro	Glu	Gly	Gly	Arg	Gln	Pro	Pro	Ile	Asp	Phe	Arg	Asp
			260					265					270		
Val	Asp	Ile	Gly	Glu	Leu	Ser	Ser	Asp	Val	Ile	Ser	Asn	Ile	Glu	Thr
		275					280					285			

Phe 290	Asp	Val	Asn	Glu	Phe	Asp 295	Gln	Tyr	Leu	Pro	Pro 300	Asn	Gly	His	Pro
Gly 305	Val	Pro	Ala	Thr	His 310	Gly	Gln	Val	Thr	Tyr 315	Thr	Gly	Ser	Tyr	Gly 320
Ile	Ser	Ser	Thr	Ala 325	Ala	Thr	Pro	Ala	Ser 330	Ala	Gly	His	Val	Trp 335	Met
Ser	Lys	Gln	Gln 340	Ala	Pro	Pro	Pro	Pro 345	Pro	Gln	Gln	Pro	Pro 350	Gln	Ala
Pro	Pro	Ala 355	Pro	Gln	Ala	Pro	Pro 360	Gln	Pro	Gln	Ala 365	Ala 365	Pro	Pro	Gln
Gln 370	Pro	Ala	Ala	Pro	Pro	Gln 375	Gln	Pro	Gln	Ala	His 380	Thr	Leu	Thr	Thr
Leu 385	Ser	Ser	Glu	Pro	Gly 390	Gln	Ser	Gln	Arg	Thr 395	His	Ile	Lys	Thr	Glu 400
Gln	Leu	Ser	Pro	Ser 405	His	Tyr	Ser	Glu 410	Gln	Gln	Gln	His	Ser	Pro 415	Gln
Gln	Ile	Ala	Tyr 420	Ser	Pro	Phe	Asn 425	Leu 425	Pro	His	Tyr	Ser 430	Pro 430	Ser	Tyr
Pro	Pro	Ile 435	Thr	Arg	Ser	Gln 440	Tyr 440	Asp	Tyr	Thr	Asp 445	His 445	Gln	Asn	Ser
Ser 450	Ser	Tyr	Tyr	Ser	His 455	Ala 455	Ala	Gly	Gln	Gly 460	Thr 460	Gly	Leu	Tyr	Ser
Thr 465	Phe	Thr	Tyr	Met 470	Asn 470	Pro	Ala	Gln	Arg	Pro 475	Met 475	Tyr	Thr	Pro	Ile 480
Ala	Asp	Thr	Ser	Gly 485	Val	Pro	Ser	Ile 490	Pro 490	Gln	Thr	His	Ser	Pro 495	Gln
His	Trp	Glu	Gln 500	Pro	Val	Tyr	Thr 505	Gln 505	Leu	Thr	Arg	Pro			